46. (New) The method of claim 43, wherein said population of RNA comprises total RNA.

47. (New) The method of claim 43, wherein said promoter sequence comprises a phage T3 promoter.

48. (New) The method of claim 43, wherein said promoter sequence comprises a phage SP6 promoter.

49. (New) The method of claim 43, wherein said promoter sequence comprises a phage T7 promoter.

50. (New) The method of claim 43, wherein said random oligomers are of a uniform length.

51. (New) The method of claim 43, wherein said random oligomers comprise hexamers.

52. (New) The method of claim 43, wherein said random oligomers are between 6 and 15 nucleotides in length.

53. (New) The method of claim 43, wherein said second strand cDNA is synthesized using the Klenow fragment of DNA polymerase I.

54. (New) The method of claim 43, wherein said second strand cDNA is synthesized using T4 DNA polymerase.

55. (New) The method of claim 43, wherein said second strand cDNA is synthesized using *E. coli* DNA polymerase I alone or in conjunction with a DNA ligase.

56. (New) The method of claim 43, wherein said first portion of said primer comprises a poly deoxythymidylate (poly dT) sequence.

57. (New) A method for analyzing a population of RNA comprising the steps of:

producing a population of cDNA from a population of RNA, wherein said method employs a primer having a first portion comprising oligo dT, and a second portion comprising a phage promoter sequence, wherein the first portion is 3' to said second portion;

synthesizing second strand cDNA complementary to said population of first strand cDNA by extending random oligomers, to form a population of double stranded cDNA;

creating a population of cRNA from said double stranded cDNA;

hybridizing the population of cRNA to an array; and

analyzing a resulting hybridization pattern.

58. (New) The method of claim 43, wherein said population of cRNA is synthesized using an RNA polymerase.

59. (New) The method of claim 57, wherein said population of cRNA is synthesized using an RNA polymerase.

60. (New) The method of claim 44, wherein said RNA is isolated from an eukaryotic cell or tissue.

61. (New) The method of claim 60, wherein said eukaryotic cell or tissue is mammalian.

62. (New) The method of claim 61, wherein said mammalian cell or tissue is human.

63. (New) The method of claim 44, wherein said RNA is isolated from a source selected from the group consisting of dissected tissue, microdissected tissue, a tissue subregion, a tissue biopsy sample, a cell sorted population, a cell culture, and a single cell.

64. (New) The method of claim 44, wherein said RNA is isolated from a cell or tissue source selected from the group consisting of brain, liver, heart, kidney, lung, spleen, retina, bone, lymph node, endocrine gland, reproductive organ, blood, nerve, vascular tissue, and olfactory epithelium.

65. (New) The method of claim 44, wherein said RNA is isolated from a cell or tissue source selected from the group consisting of embryonic and tumorigenic.

66. (New) The method of claim 43, further comprising:

labeling said population of cRNA.

67. (New) The method of claim 66, wherein said labeling is selected from the group consisting of biotinylation, fluorescent labeling, and radiolabeling.

68. (New) The method of claim 43, further comprising:

contacting said population of cRNA with a solid support comprising nucleic acid probes.

69. (New) The method of claim 43, further comprising:

detecting the presence or absence of hybridization of said population of cRNA to said nucleic acid probes on said solid support.

70. (New) The method of claim 69, wherein said solid support comprising nucleic acid probes is selected from the group consisting of a nucleic acid probe array, a membrane blot, a microwell, a bead, and a sample tube.

71. (New) The method of claim 43, wherein said first strand cDNA is synthesized using a polymerase that has reverse transcriptase activity.

72. (New) The method of claim 71, wherein said reverse transcriptase is selected from the group consisting of avian myeloblastosis virus (AMV) reverse transcriptase, Moloney murine leukemia virus (MMuLV) reverse transcriptase, and Rous Sacroma Virus (RSV) reverse transcriptase.